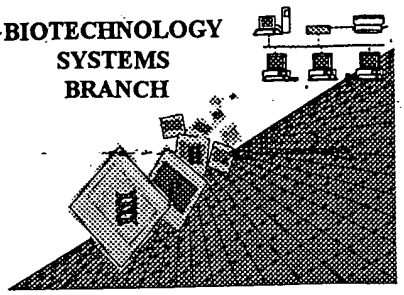
0500
#4
DT
01-220



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/657,289

Source: OIPE

Date Processed by STIC: 9/21/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/657,289

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: **(2) INFORMATION FOR SEQ ID NO:X:** **(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS") **(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:** **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. **<210> sequence id number** **<400> sequence id number** **000**
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 09/21/2000
PATENT APPLICATION: US/09/657,289 TIME: 15:11:19

Input Set : A:\Copy of 94000006.APP
Output Set: N:\CRF3\09212000\I657289.raw

Does Not Comply
Corrected Diskette Needed
pp 4-5

```
 3 <110> APPLICANT: Francis, Kevin P.
 4       Contag, Pamela R.
 5       Joh, Danny J.
 7 <120> TITLE OF INVENTION: LUCIFERASE EXPRESSION CASSETTES AND METHODS OF USE
 9 <130> FILE REFERENCE: 9400-0006P
11 <140> CURRENT APPLICATION NUMBER: US/09/657,289
12 <141> CURRENT FILING DATE: 2000-09-07
14 <160> NUMBER OF SEQ ID NOS: 26
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 6
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of Artificial Sequence: Gram-positive
25       ribosome binding site
27 <400> SEQUENCE: 1
28 aggagg                                                              6
30 <210> SEQ ID NO: 2
31 <211> LENGTH: 41
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XAF3
38 <400> SEQUENCE: 2
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41 <210> SEQ ID NO: 3
42 <211> LENGTH: 36
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XAR
49 <400> SEQUENCE: 3
50 ggcggatccg tcgacttaat ataatagcga acgttg                             36
52 <210> SEQ ID NO: 4
53 <211> LENGTH: 39
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XBF
60 <400> SEQUENCE: 4
61 gggaattctc gaggaggaga gaaagaaatg aaatttgga                          39
63 <210> SEQ ID NO: 5
64 <211> LENGTH: 37
65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
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RAW SEQUENCE LISTING DATE: 09/21/2000
PATENT APPLICATION: US/09/657,289 TIME: 15:11:20

Input Set : A:\Copy of 94000006.APP
Output Set: N:\CRF3\09212000\I657289.raw

69 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XBR
71 <400> SEQUENCE: 5
72 ggcggatccg tcgacttagg tatattccat gtggtac 37
74 <210> SEQ ID NO: 6
75 <211> LENGTH: 34
76 <212> TYPE: DNA
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XCF
82 <400> SEQUENCE: 6
83 gggaattctc gaggaggatg gcaaatatga ctaa 34
85 <210> SEQ ID NO: 7
86 <211> LENGTH: 37
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XCR
93 <400> SEQUENCE: 7
94 ggcggatccg tcgacttatg ggacaaatac aaggaac 37
96 <210> SEQ ID NO: 8
97 <211> LENGTH: 37
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XDF
104 <400> SEQUENCE: 8
105 gggaattctc gaggaggagt aaaagtatgg aaaatga 37
107 <210> SEQ ID NO: 9
108 <211> LENGTH: 37
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XDR
115 <400> SEQUENCE: 9
116 ggcggatccg tcgacttaag acagagaaat tgcttga 37
118 <210> SEQ ID NO: 10
119 <211> LENGTH: 39
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XEF
126 <400> SEQUENCE: 10
127 gggaattctc gaggaggaaa acaggtatga cttcatatg 39
129 <210> SEQ ID NO: 11
130 <211> LENGTH: 38
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer XER

RAW SEQUENCE LISTING DATE: 09/21/2000
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Input Set : A:\Copy of 94000006.APP
Output Set: N:\CRF3\09212000\I657289.raw

137 <400> SEQUENCE: 11
138 ggcggatccg tcgacttaac tatcaaacgc ttcggtta 38
140 <210> SEQ ID NO: 12
141 <211> LENGTH: 20
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: Description of Artificial Sequence: LUXA-REV
148 <400> SEQUENCE: 12
149 ccacactcct cagagatgcg 20
151 <210> SEQ ID NO: 13
152 <211> LENGTH: 6
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Description of Artificial Sequence: BamH I
158 recognition sequence
160 <400> SEQUENCE: 13
161 ggatcc 6
163 <210> SEQ ID NO: 14
164 <211> LENGTH: 37
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence: vector
170 sequence
172 <400> SEQUENCE: 14
173 ggatcctgca gatgaagcaa gaggaggact ctctatg 37
175 <210> SEQ ID NO: 15
176 <211> LENGTH: 645
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Description of Artificial Sequence: pMK4 luxABCDE
182 Sal
184 <400> SEQUENCE: 15
185 atttatctaa agatgagatt aagccaatag aacgtcatta gcaaaataaa ttatattgcg 60
186 tcctacaagc aagttcatgc ttatgtttgt agggggttat tgtggagaat aaaattattt 120
187 ccaatagaga agggatggta atcattttat agtgaaatat tatgaaattg taataattta 180
188 gatattgtaa aatctaataa gttgtaataa ttttaagggg taattataaa atttgatgat 240
189 acagtatatg attttttttgt aatcataatg tcatcaaaca tcaacctatt atacataata 300
190 aaatcgtata atgatgtagt attcataaat tcggataaaa gaatgttagg aaagttaagc 360
191 aagaggagga ttttaaagtg caaaaaaaag taattgcagc tattattggg acaagcgcga 420
192 ttagcgctgt tgcggcaact caagcaaatg cggctacaac tcacacagta aaaccgggtg 480
193 aatcagtgtg ggcaatttca aataagtatg ggatttcgat tgctaaatta aagtcattaa 540
194 acaatttaac atctaatcta attttcccaa accaagtact aaaagtatct ggctcaagta 600
195 attctacgag taatagtagc cgtccatcaa cgaactcagg tggcg 645
197 <210> SEQ ID NO: 16
198 <211> LENGTH: 671

RAW SEQUENCE LISTING DATE: 09/21/2000
PATENT APPLICATION: US/09/657,289 TIME: 15:11:20

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199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Description of Artificial Sequence: pMK4 luxABCDE
204 Sa2
206 <400> SEQUENCE: 16

see item 10 on Error Summary Sheet

W--> 207 aaaaaatgag gggtgagacg tgaaantaaa gaaagataac gtagagaagc aatcagccac 60
W--> 208 caaattgata gcaatcccnt tcatcacaga ccatgaacta agcgacttat ttcaaagtga 120
209 gtatacaaac aattcgttta gatcgcactt atttaaacat accagaatta agaagcgtat 180
210 taaattagtt gctgaaaaga attatgacca aataagttct attgaagaac aagaatttat 240
211 tggtgatttg attcaagtca atccaaatgt taaagcgcaa tcaattttag atattacatc 300
212 ggattctgtt tttcataaaa ctggaattgc gcgtggtcat gtgctgtttg ctcaggcaaa 360
213 ttcgttatgt gttgcgctaa ttaagcaacc aacagtttta actcatgaga gtagcattca 420
214 atttattgaa aaagtaaaat taaatgatac ggtaagagca gaagcacgag ttgtaaatca 480
215 aactgcaaaa cattattacg tcgaagtaaa gtcatatgtt aaacatacat tagttttcaa 540
216 aggaaatttt aaaatgtttt atgataagcg aggataaaat tatggttaaa ttagcaattg 600
217 atatgatggg tggcgacaat gcgcctgata tcgtattaga agccgtacaa aaggctgttg 660
218 aagactttaa a 671
220 <210> SEQ ID NO: 17
221 <211> LENGTH: 623
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence: pMK4 luxABCDE
227 Sa3
229 <400> SEQUENCE: 17

see item 10

W--> 230 gatgggtaag aagaaaatnc ggcatcaggg gncattngcc attcaggntg ggaactgttg 60
W--> 231 gaagggcgtc gggcggcctt ttcgntattc gcagctgcga aangggatgt gctgaaggcg 120
W--> 232 attaagttgg gtaacgccag ggtttcccag tcangcgttg taaacggcgg ccagtgaatt 180
233 cccggggatc aagccgttta agtattacga ccagtttata tcattcatgg taaaggacag 240
234 ggccttcaaa aaggtgtaca acaacatttg aaaagcataa agtgttagtg acttagaggt 300
235 ggtatgccaa ggaaggtgga tttggcgtta ccgttgcaac actaaaataa attataattt 360
236 gataaattaa atagctgcag ttaaaataat gtaaagcaac aagaatacat ttcaaacatg 420
237 ttatttgaaa taagcataaa aattgagcaa atagaaatac atgaagcatg ttatctgata 480
238 taatttgaac atcataataa taattaagga ggattggcat ttatggcaat cgtaaaagta 540
239 acagatgcag attttgattc aaaagtagaa tctggtgtac aactagtaga tttttgggca 600
240 acatggtgtg gtccatgtaa aat 623
242 <210> SEQ ID NO: 18
243 <211> LENGTH: 671
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: pMK4 luxABCDE
249 Sa4
251 <400> SEQUENCE: 18
252 gatgtatatt cacggggcac atgctgccga aaagcatcac cattaggtgc aatgtcatta 60
253 ctattgggac ggtttttata ttttattgct actcaaggtt ttgtaaatat gcaattaatc 120
254 ggtgcgatta tctttgtatt aattacaggt cctcttttca agtcatatga ttatgaaagc 180
255 agcatataat attaaaacgc cttatactaa aaagactaaa gcgatgaaat ttcggaagac 240

RAW SEQUENCE LISTING DATE: 09/21/2000
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Input Set : A:\Copy of 94000006.APP
Output Set: N:\CRF3\09212000\I657289.raw

item 10

W--> 256 ttaaaagcnc aaaattgtag attatataac aaaatcatga atataaatca acaacaaaca 300
257 gcagtaagat gattccaaat taggaatgat tttactgctg ttttcttttg acattgttac 360
258 ctctttttca atgatttttt ctttgactac agattcgccc tatctacata tatctcttta 420
259 atttaattgc ctttcatgtc gttatgtatt atgataataa taattataaa tcgtaacgat 480
260 tacgttttaa aaagagagag gttttattat gcattggaca attatcggcg gtggcataca 540
261 gggaactgca atcgcacaaa aactattatc aagcggatta acaacagacc gattaacaat 600
262 cattgaccca cacgaaactt tttgccaaag gtttaactca tatacaaatc gaatagaaat 660
263 gccttattta a 671
265 <210> SEQ ID NO: 19
266 <211> LENGTH: 650
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence: pMK4 luxABCDE
272 Sa5
274 <400> SEQUENCE: 19

item 10

W--> 275 naccagnnaa aatggtaata aaaatggcag aagnaataaa aaaaggataa agagatccca 60
W--> 276 aacggtatag agcttagtat aaaattttcg gacaataaaa taaatacggg ttnaaccnaa 120
277 ttttaacggg aaagcacttc agaatatggt gtgtttgatc aagaataaaa ttaatgatga 180
278 aaatttaacg gagaatagtg tatattgagt agatcaagaa taaaaagata attctactat 240
279 tgttgtgaag gcaaataagt agaagatttt aagtgtaatt tctggtgatt taaataataa 300
280 tataaatgga agtactgata taaaactttt taacctacta gattcttata atttgctttc 360
281 cattttatga cgatttttac tcaattgagt gatagaatca aaaaagccat ctcaaaaatt 420
282 aatcaagcaa acaacattcc aaacaatgct cgcaaatcac caatgtatca ctctccaatt 480
283 acgtaactat gatttaattt aagcatagtt attgaggttt tgtgatatat agtataaaat 540
284 taatgagaat taaatttaat aatgtaaaat tcatcttcgg ggtcgggtgt aattcccaac 600
285 cggcagtaaa taaagcctgc gacctgctag tatgtatcat attagtggct 650
287 <210> SEQ ID NO: 20
288 <211> LENGTH: 677
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Description of Artificial Sequence: pMK4 luxABCDE
294 Sa6
296 <400> SEQUENCE: 20

item 10

W--> 297 cggaagaacg ctttgaagnt taagctaatt acatctcatc atatgcacgg agatccttaa 60
W--> 298 atgccnaatt gaaagatatt tatatgaatc atcgagncng tcttgatgta gctattgcna 120
299 gcagatgata tttgtccagc aataactaat ggggaacaag tgaaaggcct ttacctttat 180
300 ggtccatttg ggcaggtaaa tcttttattc taggtgcaat tgcggaatca gctcaaatct 240
301 aagaaggtac gttcgacaat tatttattta ccgggaattt attagaacat taaaaggtgg 300
302 ctttaaagat ggttcttttg aaaagaaatt acatcgcgta agagaagcaa acattttaat 360
303 gcttgatgat attggggctg aagaagtgac tccatgggtg agagatgagg taattggacc 420
304 tttgctacat tatcgaatgg ttcatgaatt accaacattc tttagttcta attttgacta 480
305 tagtgaattg gaacatcatt tagcgatgac tcgtgatggt gaagagaaga ctaaagcagc 540
306 acgtattatt gaacgtgtca aatctttgtc aacaccatac tttttatcag gagaaaattt 600
307 cagaaacaat tgaattttaa aatgattggt gtataatgaa tacaaatcta aatcgtttaa 660
308 atgattgaag acaagat 677
310 <210> SEQ ID NO: 21
311 <211> LENGTH: 622

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 09/21/2000
PATENT APPLICATION: US/09/657,289 TIME: 15:11:21

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Output Set: N:\CRF3\09212000\I657289.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:207 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:207 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:207 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:208 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:208 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
M:340 Repeated in SeqNo=16
L:230 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:230 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:230 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:231 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:231 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
M:340 Repeated in SeqNo=17
L:232 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:232 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:256 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:256 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:256 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:275 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:275 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:275 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
L:276 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:276 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
M:340 Repeated in SeqNo=19
L:297 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:297 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:298 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
M:340 Repeated in SeqNo=20
L:320 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:320 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:320 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
L:321 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:321 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
M:340 Repeated in SeqNo=21
L:322 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:322 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:343 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:343 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:343 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
L:364 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:364 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:364 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
L:409 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:409 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:409 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25

VERIFICATION SUMMARY DATE: 09/21/2000
PATENT APPLICATION: US/09/657,289 TIME: 15:11:21

Input Set : A:\Copy of 94000006.APP
Output Set: N:\CRF3\09212000\I657289.raw

L:430 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:430 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:430 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:431 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:431 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
M:340 Repeated in SeqNo=26